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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/904,954

DATE: 07/24/2001
 TIME: 11:32:58

Input Set : N:\Crf3\RULE60\09904954.txt
 Output Set: N:\CRF3\07242001\I904954.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: BECKMANN, M. P.
 CERRETTI, DOUGLAS P.

9 (ii) TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
 RECEPTOR HEK

12 (iii) NUMBER OF SEQUENCES: 4

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: IMMUNEX CORPORATION
 16 (B) STREET: 51 UNIVERSITY STREET
 17 (C) CITY: SEATTLE
 18 (D) STATE: WASHINGTON
 19 (E) COUNTRY: USA
 20 (F) ZIP: 98101

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: Apple Macintosh
 25 (C) OPERATING SYSTEM: Apple System 7.1
 26 (D) SOFTWARE: Microsoft Word for Apple, Version 5.1a

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/904,954
 C--> 30 (B) FILING DATE: 12-Jul-2001
 31 (C) CLASSIFICATION:

41 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 08/240,124
 35 (B) FILING DATE:
 38 (A) APPLICATION NUMBER: US 08/114,426
 39 (B) FILING DATE: 30-AUG-1993
 42 (A) APPLICATION NUMBER: US 08/109,745
 43 (B) FILING DATE: 20-AUG-1993

45 (viii) ATTORNEY/AGENT INFORMATION:

46 (A) NAME: SEESE, KATHRYN A.
 47 (B) REGISTRATION NUMBER: 32,172
 48 (C) REFERENCE/DOCKET NUMBER: 2814-C

50 (ix) TELECOMMUNICATION INFORMATION:

51 (A) TELEPHONE: (206) 587-0430
 52 (B) TELEFAX: (206) 233-0644
 53 (C) TELEX: 756822

56 (2) INFORMATION FOR SEQ ID NO: 1:

58 (i) SEQUENCE CHARACTERISTICS:

59 (A) LENGTH: 1037 base pairs
 60 (B) TYPE: nucleic acid
 61 (C) STRANDEDNESS: single
 62 (D) TOPOLOGY: linear

64 (ii) MOLECULE TYPE: cDNA to mRNA

66 (iii) HYPOTHETICAL: NO

68 (iv) ANTI-SENSE: NO

ENTERED

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71 (vii) IMMEDIATE SOURCE:
72 (B) CLONE: hek-L A2
74 (ix) FEATURE:
75 (A) NAME/KEY: CDS
76 (B) LOCATION: 83..799
78 (ix) FEATURE:
79 (A) NAME/KEY: sig_peptide
80 (B) LOCATION: 83..139
82 (ix) FEATURE:
83 (A) NAME/KEY: mat_peptide
84 (B) LOCATION: 140..796
87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
89 GGATCTTGGGA ACGAGACGAC CTGCTGGAGA AGCCGGGAGC GCGGGGCTCA GTGGGGGGGC 60
91 GGCGGCCGCG CGCGCTCCGG GG ATG GCG GCG GCT CCG CTG CTG CTG CTG CTG 112
92 Met Ala Ala Ala Pro Leu Leu Leu Leu
93 -19 -15 -10
95 CTG CTC GTG CCC GTG CCG CTG CTG CCG CTG CTG GCC CAA GGG CCC GGA 160
96 Leu Leu Val Pro Val Pro Leu Leu Pro Leu Ala Gln Gly Pro Gly
97 -5 1 5
99 GGG GCG CTG GGA AAC CGG CAT GCG GTG TAC TGG AAC AGC TCC AAC CAG 208
100 Gly Ala Leu Gly Asn Arg His Ala Val Tyr Trp Asn Ser Ser Asn Gln
101 10 15 20
103 CAC CTG CGG CGA GAG GGC TAC ACC GTG CAG GTG AAC GTG AAC GAC TAT 256
104 His Leu Arg Arg Glu Gly Tyr Thr Val Gln Val Asn Val Asn Asp Tyr
105 25 30 35
107 CTG GAT ATT TAC TGC CCG CAC TAC AAC AGC TCG GGG GTG GGC CCC GGG 304
108 Leu Asp Ile Tyr Cys Pro His Tyr Asn Ser Ser Gly Val Gly Pro Gly
109 40 45 50 55
111 GCG GGA CCG GGG CCC GGA GGC GGG GCA GAG CAG TAC GTG CTG TAC ATG 352
112 Ala Gly Pro Gly Pro Gly Gly Ala Glu Gln Tyr Val Leu Tyr Met
113 60 65 70
115 GTG AGC CGC AAC GGC TAC CGC ACC TGC AAC GCC AGC CAG GGC TTC AAG 400
116 Val Ser Arg Asn Gly Tyr Arg Thr Cys Asn Ala Ser Gln Gly Phe Lys
117 75 80 85
119 CGC TGG GAG TGC AAC CGG CCG CAC GCC CCG CAC AGC CCC ATC AAG TTC 448
120 Arg Trp Glu Cys Asn Arg Pro His Ala Pro His Ser Pro Ile Lys Phe
121 90 95 100
123 TCG GAG AAG TTC CAG CGC TAC AGC GCC TTC TCT CTG GGC TAC GAG TTC 496
124 Ser Glu Lys Phe Gln Arg Tyr Ser Ala Phe Ser Leu Gly Tyr Glu Phe
125 105 110 115
127 CAC GCC GGC CAC GAG TAC TAC ATC TCC ACG CCC ACT CAC AAC CTG 544
128 His Ala Gly His Glu Tyr Tyr Ile Ser Thr Pro Thr His Asn Leu
129 120 125 130 135
131 CAC TGG AAG TGT CTG AGG ATG AAG GTG TTC GTC TGC GCC TCC ACA 592
132 His Trp Lys Cys Leu Arg Met Lys Val Phe Val Cys Cys Ala Ser Thr
133 140 145 150
135 TCG CAC TCC GGG GAG AAG CCG GTC CCC ACT CTC CCC CAG TTC ACC ATG 640
136 Ser His Ser Gly Glu Lys Pro Val Pro Thr Leu Pro Gln Phe Thr Met
137 155 160 165

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139	GGC CCC AAT GTG AAG ATC AAC GTG CTG GAA GAC TTT GAG GGA GAG AAC	688
140	Gly Pro Asn Val Lys Ile Asn Val Leu Glu Asp Phe Glu Gly Glu Asn	
141	170 175 180	
143	CCT CAG GTG CCC AAG CTT GAG AAG AGC ATC AGC GGG ACC AGC CCC AAA	736
144	Pro Gln Val Pro Lys Leu Glu Lys Ser Ile Ser Gly Thr Ser Pro Lys	
145	185 190 195	
147	CGG GAA CAC CTG CCC CTG GCC GTG GGC ATC GCC TTC TTC CTC ATG ACG	784
148	Arg Glu His Leu Pro Leu Ala Val Gly Ile Ala Phe Phe Leu Met Thr	
149	200 205 210 215	
151	TTC TTG GCC TCC TAGCTCTGCC CCCTCCCCTG GGGGGGGAGA GATGGGGCGG	836
152	Phe Leu Ala Ser	
W--> 153	220	
155	GGCTTGGAAAG GAGCAGGGAG CCTTTGGCCT CTCCAAGGGA AGCCTAGTGG GCCTAGACCC	896
157	CTCCTCCCAT GGCTAGAACGT GGGGCCTGCA CCATACATCT GTGTCCGCC CCTCTACCCC	956
159	TTCCCCCCCAC GTAGGGCACT GTAGTGGACC AAGCACGGGG ACAGCCATGG GTCCCGAGCA	1016
161	GGTCGTCTCG TTCCAAGATC C	1037
164	(2) INFORMATION FOR SEQ ID NO: 2:	
166	(i) SEQUENCE CHARACTERISTICS:	
167	(A) LENGTH: 238 amino acids	
168	(B) TYPE: amino acid	
169	(D) TOPOLOGY: linear	
171	(ii) MOLECULE TYPE: protein	
173	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
175	Met Ala Ala Ala Pro Leu Leu Leu Leu Leu Val Pro Val Pro	
176	-19 -15 -10 -5	
178	Leu Leu Pro Leu Leu Ala Gln Gly Pro Gly Gly Ala Leu Gly Asn Arg	
179	1 5 10	
181	His Ala Val Tyr Trp Asn Ser Ser Asn Gln His Leu Arg Arg Glu Gly	
182	15 20 25	
184	Tyr Thr Val Gln Val Asn Val Asn Asp Tyr Leu Asp Ile Tyr Cys Pro	
185	30 35 40 45	
187	His Tyr Asn Ser Ser Gly Val Gly Pro Gly Ala Gly Pro Gly Pro Gly	
188	50 55 60	
190	Gly Gly Ala Glu Gln Tyr Val Leu Tyr Met Val Ser Arg Asn Gly Tyr	
191	65 70 75	
193	Arg Thr Cys Asn Ala Ser Gln Gly Phe Lys Arg Trp Glu Cys Asn Arg	
194	80 85 90	
196	Pro His Ala Pro His Ser Pro Ile Lys Phe Ser Glu Lys Phe Gln Arg	
197	95 100 105	
199	Tyr Ser Ala Phe Ser Leu Gly Tyr Glu Phe His Ala Gly His Glu Tyr	
200	110 115 120 125	
202	Tyr Tyr Ile Ser Thr Pro Thr His Asn Leu His Trp Lys Cys Leu Arg	
203	130 135 140	
205	Met Lys Val Phe Val Cys Cys Ala Ser Thr Ser His Ser Gly Glu Lys	
206	145 150 155	
208	Pro Val Pro Thr Leu Pro Gln Phe Thr Met Gly Pro Asn Val Lys Ile	
209	160 165 170	
211	Asn Val Leu Glu Asp Phe Glu Gly Glu Asn Pro Gln Val Pro Lys Leu	
212	175 180 185	

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214 Glu Lys Ser Ile Ser Gly Thr Ser Pro Lys Arg Glu His Leu Pro Leu
215 190 195 200 205
217 Ala Val Gly Ile Ala Phe Phe Leu Met Thr Phe Leu Ala Ser
218 210 215
221 (2) INFORMATION FOR SEQ ID NO: 3:
223 (i) SEQUENCE CHARACTERISTICS:
224 (A) LENGTH: 636 base pairs
225 (B) TYPE: nucleic acid
226 (C) STRANDEDNESS: single
227 (D) TOPOLOGY: linear
229 (iii) MOLECULE TYPE: cDNA to mRNA
231 (iii) HYPOTHETICAL: NO
233 (iv) ANTI-SENSE: NO
236 (vii) IMMEDIATE SOURCE:
237 (B) CLONE: hek-L C6
239 (ix) FEATURE:
240 (A) NAME/KEY: mat_peptide
241 (B) LOCATION: 94..630
243 (ix) FEATURE:
244 (A) NAME/KEY: CDS
245 (B) LOCATION: 28..633
247 (ix) FEATURE:
248 (A) NAME/KEY: sig_peptide
249 (B) LOCATION: 28..93
252 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
254 GCCAGACCAA ACCGGACCTC GGGGGCG ATG CGG CTG CTG CCC CTG CTG CGG 51
255 Met Arg Leu Leu Pro Leu Leu Arg
256 -22 -20 -15
258 ACT GTC CTC TGG GCC GCG TTC CTC GGC TCC CCT CTG CGC GGG GGC TCC 99
259 Thr Val Leu Trp Ala Ala Phe Leu Gly Ser Pro Leu Arg Gly Gly Ser
260 -10 -5 1
262 AGC CTC CGC CAC GTA GTC TAC TGG AAC TCC AGT AAC CCC AGG TTG CTT 147
263 Ser Leu Arg His Val Val Tyr Trp Asn Ser Ser Asn Pro Arg Leu Leu
264 5 10 15
266 CGA GGA GAC GCC GTG GTG GAG CTG GGC CTC AAC GAT TAC CTA GAC ATT 195
267 Arg Gly Asp Ala Val Val Glu Leu Gly Leu Asn Asp Tyr Leu Asp Ile
268 20 25 30
270 GTC TGC CCC CAC TAC GAA GGC CCA GGG CCC CCT GAG GGC CCC GAG ACG 243
271 Val Cys Pro His Tyr Glu Gly Pro Gly Pro Pro Glu Gly Pro Glu Thr
272 35 40 45 50
274 TTT GCT TTG TAC ATG GTG GAC TGG CCA GGC TAT GAG TCC TGC CAG GCA 291
275 Phe Ala Leu Tyr Met Val Asp Trp Pro Gly Tyr Glu Ser Cys Gln Ala
276 55 60 65
278 GAG GGC CCC CGG GCC TAC AAG CGC TGG GTG TGC TCC CTG CCC TTT GGC 339
279 Glu Gly Pro Arg Ala Tyr Lys Arg Trp Val Cys Ser Leu Pro Phe Gly
280 70 75 80
282 CAT GTT CAA TTC TCA GAG AAG ATT CAG CGC TTC ACA CCT TTC TCC CTC 387
283 His Val Gln Phe Ser Glu Lys Ile Gln Arg Phe Thr Pro Phe Ser Leu
284 85 90 95

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286	GGC TTT GAG TTC TTA CCT GGA GAG ACT TAC TAC TAC ATC TCG GTG CCC	435
287	Gly Phe Glu Phe Leu Pro Gly Glu Thr Tyr Tyr Tyr Ile Ser Val Pro	
288	100 105 110	
290	ACT CCA GAG AGT TCT GGC CAG TGC TTG AGG CTC CAG GTG TCT GTC TGC	483
291	Thr Pro Glu Ser Ser Gly Gln Cys Leu Arg Leu Gln Val Ser Val Cys	
292	115 120 125 130	
294	TGC AAG GAG AGG AAG TCT GAG TCA GCC CAT CCT GTT GGG AGC CCT GGA	531
295	Cys Lys Glu Arg Lys Ser Glu Ser Ala His Pro Val Gly Ser Pro Gly	
296	135 140 145	
298	GAG AGT GGC ACA TCA GGG TGG CGA GGG GAC ACT CCC AGC CCC CTC	579
299	Glu Ser Gly Thr Ser Gly Trp Arg Gly Gly Asp Thr Pro Ser Pro Leu	
300	150 155 160	
302	TGT CTC TTG CTA TTA CTG CTG CTT CTG ATT CTT CGT CTT CTG CGA ATT	627
303	Cys Leu Leu Leu Leu Leu Leu Ile Leu Arg Leu Leu Arg Ile	
304	165 170 175	
306	CTG TGAGCC	636
307	Leu	

W--> 308 180

312 (2) INFORMATION FOR SEQ ID NO: 4:

314 (i) SEQUENCE CHARACTERISTICS:

315 (A) LENGTH: 201 amino acids

316 (B) TYPE: amino acid

317 (D) TOPOLOGY: linear

319 (ii) MOLECULE TYPE: protein

321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

323	Met Arg Leu Leu Pro Leu Leu Arg Thr Val Leu Trp Ala Ala Phe Leu	
324	-22 -20 -15 -10	
326	Gly Ser Pro Leu Arg Gly Gly Ser Ser Leu Arg His Val Val Tyr Trp	
327	-5 1 5 10	
329	Asn Ser Ser Asn Pro Arg Leu Leu Arg Gly Asp Ala Val Val Glu Leu	
330	15 . 20 25	
332	Gly Leu Asn Asp Tyr Leu Asp Ile Val Cys Pro His Tyr Glu Gly Pro	
333	30 35 40	
335	Gly Pro Pro Glu Gly Pro Glu Thr Phe Ala Leu Tyr Met Val Asp Trp	
336	45 50 55	
338	Pro Gly Tyr Glu Ser Cys Gln Ala Glu Gly Pro Arg Ala Tyr Lys Arg	
339	60 65 70	
341	Trp Val Cys Ser Leu Pro Phe Gly His Val Gln Phe Ser Glu Lys Ile	
342	75 80 85 90	
344	Gln Arg Phe Thr Pro Phe Ser Leu Gly Phe Glu Phe Leu Pro Gly Glu	
345	95 100 105	
347	Thr Tyr Tyr Tyr Ile Ser Val Pro Thr Pro Glu Ser Ser Gly Gln Cys	
348	110 115 120	
350	Leu Arg Leu Gln Val Ser Val Cys Cys Lys Glu Arg Lys Ser Glu Ser	
351	125 130 135	
353	Ala His Pro Val Gly Ser Pro Gly Glu Ser Gly Thr Ser Gly Trp Arg	
354	140 145 150	
356	Gly Gly Asp Thr Pro Ser Pro Leu Cys Leu Leu Leu Leu Leu Leu	
357	155 160 165 170	

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/904,954

DATE: 07/24/2001
TIME: 11:32:59

Input Set : N:\Crf3\RULE60\09904954.txt
Output Set: N:\CRF3\07242001\I904954.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:153 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:308 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3